PENDING CLAIMS

1. A method to detect a NF-κB related medical condition in an organism comprising the steps of:

   obtaining a sample from said organism; and

   analyzing said sample for an alteration in a nucleic acid of SEQ ID NO:1, wherein said alteration results in inactivation of NF-κB.

2. The method of Claim 1, wherein said alteration is a mutation, wherein said mutation is selected from the group consisting of a deletion, an insertion, a point mutation, a rearrangement in said sequence, and a combination thereof.

3. The method of Claim 2, wherein said point mutation is selected from the group consisting of a nonsense mutation, a frameshift mutation, a missense mutation, a splicing-related mutation, and a combination thereof.

4. The method of Claim 1, wherein said alteration is located in a regulatory nucleic acid, a promoter nucleic acid an exon, an intron, an initiator codon, a stop codon, an exon/intron junction, a 5′ untranslated region, a 3′ untranslated region and a combination thereof.

5. The method of Claim 1, wherein said analyzing step comprises a method selected from the group consisting of hybridization, SSCP, heteroduplex analysis, sequencing, polymerase chain reaction, electrophoresis, and a combination thereof.

6. The method of Claim 1, wherein said organism is a human.

7. The method of Claim 1, wherein said NF-κB related medical condition is a NF-κB Essential Modulator related medical condition.

8. The method of Claim 1 or 7, wherein said medical condition is Incontinentia Pigmenti.

32. A method to detect an alteration in a nucleic acid of SEQ ID NO:1 in an organism, comprising the steps of:

   obtaining a sample from said organism; and

analyzing said sample for said alteration.

33. The method of Claim 32, wherein said alteration is a mutation, wherein said mutation is selected from the group consisting of a deletion, an insertion, point mutation, a rearrangement, and a combination thereof.

34. The method of Claim 33, wherein said point mutation is selected from the group consisting of a nonsense mutation, a frameshift mutation, a missense mutation, a splicing-related mutation, and a combination thereof.

35. The method of Claim 32, wherein said alteration is located in a regulatory nucleic acid, a promoter nucleic acid, an exon, an intron, an initiator codon, a stop codon, an exon/intron junction, a 5′ untranslated region, a 3′ untranslated region and a combination thereof.

36. The method of Claim 32, wherein said analyzing step comprises a method selected from the group consisting of hybridization, SSCP, heteroduplex analysis, sequencing, polymerase chain reaction, electrophoresis, and a combination thereof.

37. The method of Claim 32, wherein said organism is a human.

38. The method of Claim 32, wherein said organism is a human selected from the group consisting of an affected individual, a carrier individual, or a noncarrier individual.

39. The method of claim 32, wherein said analyzing step further comprises a technique selected from the group consisting of PCR analysis and Southern blot analysis.

43. The method of Claim 39, wherein a probe for said Southern analysis is a nucleic acid of SEQ ID NO:3, or fragments and derivatives thereof.